



## SEQUENCE LISTING

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TECH CENTER 1600/2300

<110> Hope, R. D., Graham  
Mclauchlan, John

<120> VIRAL THERAPEUTICS

<130> DYOU17.001AUS

<140> 09/201916

<141> 1998-12-01

<160> 13

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 630

<212> DNA

<213> Hepatitis C Virus

<220>

<221> CDS

<222> (43)...(630)

<400> 1

ggtgcttgcg agtgccccgg gaggtctcgt agaccgtgca cc atg agc acg aat 54  
Met Ser Thr Asn  
1

cct aaa cct caa aga aaa acc aaa cgt aac acc aac cgt cgc cca cag 102  
Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn Arg Arg Pro Gln  
5 10 15 20

gac gtt aag ttc ccg ggt ggc ggt cag atc gtt ggt gga gtt tac ttg 150  
Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly Gly Val Tyr Leu  
25 30 35

ttg ccg cgc agg ggc cct aga ttg ggt gtg cgc gcg acg agg aag act 198  
Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala Thr Arg Lys Thr  
40 45 50

tcc gag cgg tcg caa cct cga ggt aga cgt cag cct atc ccc aag gca 246  
Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Ala  
55 60 65

cgt cgg ccc aag ggc agg aac tgg gct cag ccc ggg tat cct tgg ccc 294  
Arg Arg Pro Lys Gly Arg Asn Trp Ala Gln Pro Gly Tyr Pro Trp Pro  
70 75 80

ctc tat ggc aat gag ggt tgc ggg tgg gcg gga tgg ctc ctg tcc ccc 342  
Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp Leu Leu Ser Pro  
85 90 95 100

agt ggc tct cgg cct agt tgg ggc ccc aac gac ccc cga cgt agg tcg	390
Ser Gly Ser Arg Pro Ser Trp Gly Pro Asn Asp Pro Arg Arg Arg Ser	
105 110 115	

cgc aat ttg ggt aag gtc atc gat acc ctt acg tgc ggc ttc gtc gat	438
Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Val Asp	
120 125 130	

ctc atg ggg tac ata ccg ctc gtc ggc gcc cct ctt aga ggc gct gcc	486
Leu Met Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu Arg Gly Ala Ala	
135 140 145	

agg gcc ctg gcg cat ggc gtc cgg gtt ctg gaa gac ggt gtg aac tat	534
Arg Ala Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr	
150 155 160	

gca aca ggt aac ctt cct ggt tgc tct ttc tct atc ttc ctt ctg gcc	582
Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala	
165 170 175 180	

ctg ctc tct tgc ctg act gtg ccc gct tca gcc tac caa gtg cgc aac	630
Leu Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Tyr Gln Val Arg Asn	
185 190 195	

<210> 2  
 <211> 60  
 <212> DNA  
 <213> Hepatitis C Virus

<220>  
 <221> CDS  
 <222> (1)...(60)  
 <223> Corresponds to aa 125 to 144 of SEQ ID. No. 1

<400> 2	
acc ctt acg tgc ggc ttc gtc gat ctc atg ggg tac ata ccg ctc gtc	48
Thr Leu Thr Cys Gly Phe Val Asp Leu Met Gly Tyr Ile Pro Leu Val	
1 5 10 15	

ggc gcc cct ctt	60
Gly Ala Pro Leu	
20	

<210> 3  
 <211> 18  
 <212> DNA  
 <213> Hepatitis C Virus

<220>  
 <221> CDS  
 <222> (1)...(18)  
 <223> Corresponds to aa 161-166 of SEQ ID. No. 1

<400> 3

ggt gtg aac tat gca aca

Gly Val Asn Tyr Ala Thr

1

5

18

<210> 4

<211> 1900

<212> DNA

<213> Human

<220>

<221> misc\_feature

<222> (1)...(1900)

<223> n = A,T,C or G

<400> 4

cgtcttcggg	acgcgccgc	tcttcgcctt	tcgctgcagt	ccgtcgattt	ctttctccag	60
gaagaaaaat	ggcatccgtt	gcagttgac	cacaaccgag	tgtggtgact	cgggtggtca	120
acctgccctt	ggtgagctcc	acgtatgacc	tcattgtcctc	agcctatctc	agtacaaagg	180
accagtatcc	ctacctgaag	tctgtgtgtg	agatgscaga	gaacgggtgtg	aagaccatca	240
cctccgtggc	catgaccagt	gctctgccca	tcattccagaa	gctagagccg	caaattgcag	300
ttgccgatac	ctatgcctgt	aaggggctag	acaggattga	ggagagactg	cctattctga	360
atcagccatc	aactcagatt	gttgccaatg	ccaaaggcgc	tgtgactggg	gcaaaagatg	420
ctgtgacgac	tactgtgact	ggggccaagg	attctgtngc	cagcacgac	acaggggtga	480
tggacaagac	caaaggggca	gtgactggca	gtgtggagaa	gaccaagtct	gtggtcagt	540
gcagcattaa	cacagtcttg	gggagtcgga	tgatgcagct	cgtgagcagt	ggcgtagaaa	600
atgcactcac	caaatacagag	ctgttggtag	aacagtacct	ccctctcact	gaggaagaac	660
tagaaaaaga	agcaaaaaaa	gttgaaggat	ttgatctggg	tcagaagcca	agttattatg	720
ttagactggg	atccctgtct	accaagcttc	actcccgctg	ctaccagcag	gctctcagca	780
gggttaaaga	agctaagcaa	aaaagccaac	agaccatttc	tcagctccat	tctactgttc	840
acctgattga	atttgccagg	aagaatgtgt	atagtgccaa	tcagaaaatt	caggatgctc	900
aggataagct	ctacctctca	tgggtagagt	ggaaaaggag	cattggatat	gatgatactg	960
atgagtccca	ctgtgctgag	cacattgagt	cacgtactct	tgcaattgcc	cgcaacctga	1020
ctcagcagct	ccagaccacg	tgccacaccc	tcctgtccaa	catccaaggt	gtaccacaga	1080
acatccaaga	tcaagccaag	cacatggggg	tgatggcagg	cgacatctac	tcagtgttcc	1140
gcaatgctgc	ctcctttaaa	gaagtgtctg	acagcctcct	cacttctagc	aaggggcagc	1200
tgcagaaaat	gaaggaatct	ttagatgacg	tgatggatta	tcttgttaac	aacacgcccc	1260
tcaactggct	ggtaggtccc	ttttatectc	agctgactga	gtctcagaat	gctcaggacc	1320
aagggtgcaga	gatggacaag	agcagccagg	agaccagcgc	atctgagcat	aaaactcatt	1380
aaacctgccc	ctatcactag	tgcatgctgt	ggccagacag	atgacacctt	ttgttatgtt	1440
gaaattaact	tgctaggcaa	ccctaaattg	ggaagcaagt	agctagtata	aaggccctca	1500
attgtagttg	tttccagctg	aattaagagc	tttaaagttt	ctggcattag	cagatgattt	1560
ctgttcacct	ggtaagaaaa	gaatgatagg	cttgtcagag	cctatagcca	gaactcagaa	1620
aaaattcaaa	tgcacttatg	ttctcattct	atggccattg	tggtgcctct	gttactgttt	1680
gtattgaata	aaaacatctt	catgtgggct	ggggtagaaa	ctgggtgtctg	ctctgggtgtg	1740
atctgaaaag	gcgtcttcac	tgctttatct	catgatgctt	gcttgtaaaa	cttgatttta	1800
gtttttcatt	tctcaaatag	gaatactacc	tttgaattca	ataaaattca	ctgcaggata	1860
gaccagttna	gnagcaaaca	nncangtaca	cnnaaganac			1900

<210> 5

<211> 437

<212> PRT

<213> Human

<220>

<221> VARIANT

<222> (1)...(437)

<223> Xaa = Any Amino Acid

<400> 5

Met	Ala	Ser	Val	Ala	Val	Asp	Pro	Gln	Pro	Ser	Val	Val	Thr	Arg	Val
1				5					10					15	
Val	Asn	Leu	Pro	Leu	Val	Ser	Ser	Thr	Tyr	Asp	Leu	Met	Ser	Ser	Ala
			20					25					30		
Tyr	Leu	Ser	Thr	Lys	Asp	Gln	Tyr	Pro	Tyr	Leu	Lys	Ser	Val	Cys	Glu
		35					40					45			
Met	Xaa	Glu	Asn	Gly	Val	Lys	Thr	Ile	Thr	Ser	Val	Ala	Met	Thr	Ser
	50					55					60				
Ala	Leu	Pro	Ile	Ile	Gln	Lys	Leu	Glu	Pro	Gln	Ile	Ala	Val	Ala	Asp
65					70					75					80
Thr	Tyr	Ala	Cys	Lys	Gly	Leu	Asp	Arg	Ile	Glu	Glu	Arg	Leu	Pro	Ile
				85					90					95	
Leu	Asn	Gln	Pro	Ser	Thr	Gln	Ile	Val	Ala	Asn	Ala	Lys	Gly	Ala	Val
			100					105					110		
Thr	Gly	Ala	Lys	Asp	Ala	Val	Thr	Thr	Thr	Val	Thr	Gly	Ala	Lys	Asp
		115					120					125			
Ser	Val	Ala	Ser	Thr	Ile	Thr	Gly	Val	Met	Asp	Lys	Thr	Lys	Gly	Ala
	130					135					140				
Val	Thr	Gly	Ser	Val	Glu	Lys	Thr	Lys	Ser	Val	Val	Ser	Gly	Ser	Ile
145					150					155					160
Asn	Thr	Val	Leu	Gly	Ser	Arg	Met	Met	Gln	Leu	Val	Ser	Ser	Gly	Val
				165					170					175	
Glu	Asn	Ala	Leu	Thr	Lys	Ser	Glu	Leu	Leu	Val	Glu	Gln	Tyr	Leu	Pro
		180						185					190		
Leu	Thr	Glu	Glu	Glu	Leu	Glu	Lys	Glu	Ala	Lys	Lys	Val	Glu	Gly	Phe
		195					200					205			
Asp	Leu	Val	Gln	Lys	Pro	Ser	Tyr	Tyr	Val	Arg	Leu	Gly	Ser	Leu	Ser
	210					215					220				
Thr	Lys	Leu	His	Ser	Arg	Ala	Tyr	Gln	Gln	Ala	Leu	Ser	Arg	Val	Lys
225					230					235					240
Glu	Ala	Lys	Gln	Lys	Ser	Gln	Gln	Thr	Ile	Ser	Gln	Leu	His	Ser	Thr
				245					250					255	
Val	His	Leu	Ile	Glu	Phe	Ala	Arg	Lys	Asn	Val	Tyr	Ser	Ala	Asn	Gln
		260						265					270		
Lys	Ile	Gln	Asp	Ala	Gln	Asp	Lys	Leu	Tyr	Leu	Ser	Trp	Val	Glu	Trp
		275					280					285			
Lys	Arg	Ser	Ile	Gly	Tyr	Asp	Asp	Thr	Asp	Glu	Ser	His	Cys	Ala	Glu
	290					295					300				
His	Ile	Glu	Ser	Arg	Thr	Leu	Ala	Ile	Ala	Arg	Asn	Leu	Thr	Gln	Gln
305					310					315					320
Leu	Gln	Thr	Thr	Cys	His	Thr	Leu	Leu	Ser	Asn	Ile	Gln	Gly	Val	Pro
				325					330					335	
Gln	Asn	Ile	Gln	Asp	Gln	Ala	Lys	His	Met	Gly	Val	Met	Ala	Gly	Asp
		340						345					350		
Ile	Tyr	Ser	Val	Phe	Arg	Asn	Ala	Ala	Ser	Phe	Lys	Glu	Val	Ser	Asp
		355					360					365			
Ser	Leu	Leu	Thr	Ser	Ser	Lys	Gly	Gln	Leu	Gln	Lys	Met	Lys	Glu	Ser
	370						375					380			

Leu Asp Asp Val Met Asp Tyr Leu Val Asn Asn Thr Pro Leu Asn Trp  
 385 390 395 400  
 Leu Val Gly Pro Phe Tyr Pro Gln Leu Thr Glu Ser Gln Asn Ala Gln  
 405 410 415  
 Asp Gln Gly Ala Glu Met Asp Lys Ser Ser Gln Glu Thr Gln Arg Ser  
 420 425 430  
 Glu His Lys Thr His  
 435

<210> 6  
 <211> 31  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> A branched peptide containing residues 5-27 of the  
 HCV core protein.

<221> VARIANT  
 <222> (1)...(31)  
 <223> Xaa = Ala or Pro at position 1, and Ile or Asn at  
 position 12.

<400> 6  
 Xaa Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Xaa Arg Arg Pro Gln  
 1 5 10 15  
 Asp Val Lys Phe Pro Gly Gly Lys Lys Lys Lys Lys Lys Ala  
 20 25 30

<210> 7  
 <211> 11  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Oligonucleotides used to construct HCV core  
 protein deletion plasmids.

<400> 7  
 gctgagatct a

11

<210> 8  
 <211> 29  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Oligonucleotides used to construct HCV core  
 protein deletion plasmids.

<400> 8  
 gtaaccttcc tgggttgctct tgagatcta

29

<210> 9  
 <211> 17

<212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Oligonucleotides used to construct HCV core  
           protein deletion plasmids.  
  
 <400> 9  
 gtaacctttg agatcta 17  
  
 <210> 10  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Oligonucleotides used to construct HCV core  
           protein deletion plasmids.  
  
 <400> 10  
 ctggcgcatt gagatcta 18  
  
 <210> 11  
 <211> 28  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Oligonucleotides used to construct HCV core  
           protein deletion plasmids.  
  
 <400> 11  
 ctggcccatg gtgttaacta tgcaacag 28  
  
 <210> 12  
 <211> 31  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Oligonucleotides used to construct HCV core  
           protein deletion plasmids.  
  
 <400> 12  
 ctggcccatg gcgtccgggt tctggaagac g 31  
  
 <210> 13  
 <211> 37  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Oligonucleotides used to construct HCV core  
           protein deletion plasmids.

<400> 13

cgatagaggc gctgccaggg ccctggcgtg agatcta

37

c'